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Page 1 of 7

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P#18

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1600

RAW SEQUENCE LISTING

DATE: 06/17/2003

PATENT APPLICATION: US/09/508,849A

TIME: 07:40:19

Input Set : A:\2003-06-09 1110-0266P.ST25.txt

Output Set: N:\CRF4\06172003\I508849A.raw

3 <110> APPLICANT: NAGATA, Shigekazu
4 TANAKA, Masato
6 <120> TITLE OF INVENTION: Novel Fas Ligand Derivative
8 <130> FILE REFERENCE: 1110-0266P
10 <140> CURRENT APPLICATION NUMBER: 09/508,849A
11 <141> CURRENT FILING DATE: 2001-03-17
13 <150> PRIOR APPLICATION NUMBER: PCT/JP98/04187
14 <151> PRIOR FILING DATE: 1998-09-17
16 <150> PRIOR APPLICATION NUMBER: JP 9-252541
17 <151> PRIOR FILING DATE: 1997-09-17
19 <160> NUMBER OF SEQ ID NOS: 17
21 <170> SOFTWARE: PatentIn version 3.2
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 258
25 <212> TYPE: PRT
26 <213> ORGANISM: Artificial Sequence
28 <220> FEATURE:
29 <223> OTHER INFORMATION: Description of Artificial Sequence: amino acids at
30 111-133 from N terminal are deleted from natural
31 human Fas ligand
33 <400> SEQUENCE: 1
34 Met Gln Gln Pro Phe Asn Tyr Pro Tyr Pro Gln Ile Tyr Trp Val Asp
35 1 5 10 15
37 Ser Ser Ala Ser Ser Pro Trp Ala Pro Pro Gly Thr Val Leu Pro Cys
38 20 25 30
40 Pro Thr Ser Val Pro Arg Arg Pro Gly Gln Arg Arg Pro Pro Pro Pro
41 35 40 45
43 Pro Pro Pro Pro Leu Pro Pro Pro Pro Pro Pro Pro Pro Leu Pro
44 50 55 60
46 Pro Leu Pro Leu Pro Pro Leu Lys Lys Arg Gly Asn His Ser Thr Gly
47 65 70 75 80
49 Leu Cys Leu Leu Val Met Phe Phe Met Val Leu Val Ala Leu Val Gly
50 85 90 95
52 Leu Gly Leu Gly Met Phe Gln Leu Phe His Leu Gln Lys Glu Pro Ser
53 100 105 110
55 Pro Pro Pro Glu Lys Lys Glu Leu Arg Lys Val Ala His Leu Thr Gly
56 115 120 125
58 Lys Ser Asn Ser Arg Ser Met Pro Leu Glu Trp Glu Asp Thr Tyr Gly
59 130 135 140
61 Ile Val Leu Leu Ser Gly Val Lys Tyr Lys Lys Gly Gly Leu Val Ile
62 145 150 155 160
64 Asn Glu Thr Gly Leu Tyr Phe Val Tyr Ser Lys Val Tyr Phe Arg Gly
65 165 170 175

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67 Gln Ser Cys Asn Asn Leu Pro Leu Ser His Lys Val Tyr Met Arg Asn
68           180          185          190
70 Ser Lys Tyr Pro Gln Asp Leu Val Met Met Glu Gly Lys Met Met Ser
71           195          200          205
73 Tyr Cys Thr Thr Gly Gln Met Trp Ala Arg Ser Ser Tyr Leu Gly Ala
74           210          215          220
76 Val Phe Asn Leu Thr Ser Ala Asp His Leu Tyr Val Asn Val Ser Glu
77 225          230          235          240
79 Leu Ser Leu Val Asn Phe Glu Glu Ser Gln Thr Phe Phe Gly Leu Tyr
80           245          250          255
82 Lys Leu
86 <210> SEQ ID NO: 2
87 <211> LENGTH: 277
88 <212> TYPE: PRT
89 <213> ORGANISM: Artificial Sequence
91 <220> FEATURE:
92 <223> OTHER INFORMATION: Description of Artificial Sequence: amino acids at
93   128-131 from N terminal are deleted from natural
94   human Fas ligang
96 <400> SEQUENCE: 2
97 Met Gln Gln Pro Phe Asn Tyr Pro Tyr Pro Gln Ile Tyr Trp Val Asp
98   1           5           10          15
100 Ser Ser Ala Ser Ser Pro Trp Ala Pro Pro Gly Thr Val Leu Pro Cys
101          20          25          30
103 Pro Thr Ser Val Pro Arg Arg Pro Gly Gln Arg Arg Pro Pro Pro Pro
104          35          40          45
106 Pro Pro Pro Pro Leu Pro Pro Pro Pro Pro Pro Pro Pro Leu Pro
107          50          55          60
109 Pro Leu Pro Leu Pro Pro Leu Lys Lys Arg Gly Asn His Ser Thr Gly
110          65          70          75          80
112 Leu Cys Leu Leu Val Met Phe Phe Met Val Leu Val Ala Leu Val Gly
113          85          90          95
115 Leu Gly Leu Gly Met Phe Gln Leu Phe His Leu Gln Lys Glu Leu Ala
116          100         105         110
118 Glu Leu Arg Glu Ser Thr Ser Gln Met His Thr Ala Ser Ser Leu Gly
119          115         120         125
121 His Pro Ser Pro Pro Glu Lys Lys Glu Leu Arg Lys Val Ala His
122          130         135         140
124 Leu Thr Gly Lys Ser Asn Ser Arg Ser Met Pro Leu Glu Trp Glu Asp
125          145         150         155         160
127 Thr Tyr Gly Ile Val Leu Leu Ser Gly Val Lys Tyr Lys Lys Gly Gly
128          165         170         175
130 Leu Val Ile Asn Glu Thr Gly Leu Tyr Phe Val Tyr Ser Lys Val Tyr
131          180         185         190
133 Phe Arg Gly Gln Ser Cys Asn Asn Leu Pro Leu Ser His Lys Val Tyr
134          195         200         205
136 Met Arg Asn Ser Lys Tyr Pro Gln Asp Leu Val Met Met Glu Gly Lys
137          210         215         220
139 Met Met Ser Tyr Cys Thr Thr Gly Gln Met Trp Ala Arg Ser Ser Tyr

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140 225 230 235 240
 142 Leu Gly Ala Val Phe Asn Leu Thr Ser Ala Asp His Leu Tyr Val Asn
 143 245 250 255
 145 Val Ser Glu Leu Ser Leu Val Asn Phe Glu Glu Ser Gln Thr Phe Phe
 146 260 265 270
 148 Gly Leu Tyr Lys Leu
 149 275
 152 <210> SEQ ID NO: 3
 153 <211> LENGTH: 281
 154 <212> TYPE: PRT
 155 <213> ORGANISM: Artificial Sequence
 157 <220> FEATURE:
 158 <223> OTHER INFORMATION: Description of Artificial Sequence: point mutation
 159 of a substitution of Lys 129 for Ala from N
 160 terminal is present in natural human Fas ligand
 161
 163 <400> SEQUENCE: 3
 164 Met Gln Gln Pro Phe Asn Tyr Pro Tyr Pro Gln Ile Tyr Trp Val Asp
 165 1 5 10 15
 167 Ser Ser Ala Ser Ser Pro Trp Ala Pro Pro Gly Thr Val Leu Pro Cys
 168 20 25 30
 170 Pro Thr Ser Val Pro Arg Arg Pro Gly Gln Arg Arg Pro Pro Pro Pro
 171 35 40 45
 173 Pro Pro Pro Pro Leu Pro Pro Pro Pro Pro Pro Pro Pro Leu Pro
 174 50 55 60
 176 Pro Leu Pro Leu Pro Pro Leu Lys Lys Arg Gly Asn His Ser Thr Gly
 177 65 70 75 80
 179 Leu Cys Leu Leu Val Met Phe Phe Met Val Leu Val Ala Leu Val Gly
 180 85 90 95
 182 Leu Gly Leu Gly Met Phe Gln Leu Phe His Leu Gln Lys Glu Leu Ala
 183 100 105 110
 185 Glu Leu Arg Glu Ser Thr Ser Gln Met His Thr Ala Ser Ser Leu Glu
 186 115 120 125
 188 Ala Gln Ile Gly His Pro Ser Pro Pro Glu Lys Lys Glu Leu Arg
 189 130 135 140
 191 Lys Val Ala His Leu Thr Gly Lys Ser Asn Ser Arg Ser Met Pro Leu
 192 145 150 155 160
 194 Glu Trp Glu Asp Thr Tyr Gly Ile Val Leu Leu Ser Gly Val Lys Tyr
 195 165 170 175
 197 Lys Lys Gly Gly Leu Val Ile Asn Glu Thr Gly Leu Tyr Phe Val Tyr
 198 180 185 190
 200 Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys Asn Asn Leu Pro Leu Ser
 201 195 200 205
 203 His Lys Val Tyr Met Arg Asn Ser Lys Tyr Pro Gln Asp Leu Val Met
 204 210 215 220
 206 Met Glu Gly Lys Met Met Ser Tyr Cys Thr Thr Gly Gln Met Trp Ala
 207 225 230 235 240
 209 Arg Ser Ser Tyr Leu Gly Ala Val Phe Asn Leu Thr Ser Ala Asp His
 210 245 250 255

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Input Set : A:\2003-06-09 1110-0266P.ST25.txt

Output Set: N:\CRF4\06172003\1508849A.raw

212 Leu Tyr Val Asn Val Ser Glu Leu Ser Leu Val Asn Phe Glu Glu Ser
213 260 265 270
215 Gln Thr Phe Phe Gly Leu Tyr Lys Leu
216 275 280
219 <210> SEQ ID NO: 4
220 <211> LENGTH: 774
221 <212> TYPE: DNA
222 <213> ORGANISM: Artificial Sequence
224 <220> FEATURE:
225 <223> OTHER INFORMATION: Description of Artificial Sequence:DNA coding for
226 amino acids SEQ ID No.1
228 <400> SEQUENCE: 4
229 atgcagcagc cttcaatta cccatatccc cagatctact gggtgacag cagtccagc 60
230 tctccctggg cccctccagg cacagttctt ccctgtccaa cctctgtgcc cagaaggcct 120
231 ggtcaaagga ggccaccacc accaccgcca ccgcaccac taccacctcc gccgcgcgg 180
232 ccaccactgc ctccactacc gctgccaccc ctgaagaaga gagggAACCA cagcacaggc 240
233 ctgtgtctcc ttgtatgtt ttcatgtt ctgggtgcct tgtaggatt gggctgggg 300
234 atgttcagc tctccaccc acagaaggag cccagtcac cccctgaaaa aaaggagctg 360
235 agggaaagtgg cccatttaac agcagtc aactcaaggt ccatgcctc ggaatggaa 420
236 gacacctatg gaattgtcct gcttctgga gtgaagtata agaagggtgg ctttgtatc 480
237 aatgaaactg ggctgtactt tgatattcc aaagtatact tccgggtca atcttgcac 540
238 aacctgcccc tgagccacaa ggtctacatg aggaactcta agtatcccc gatctggg 600
239 atgatggagg ggaagatgtat gagctactgc actactggc agatgtggc ccgcagcagc 660
240 tacctggggg cagtgttcaa tcttaccatg gctgatcatt tatatgtcaa cgtatcttag 720
241 ctctctctgg tcaattttga ggaatctcg acgttttcg gcttatataa gtc 774
244 <210> SEQ ID NO: 5
245 <211> LENGTH: 831
246 <212> TYPE: DNA
247 <213> ORGANISM: Artificial Sequence
249 <220> FEATURE:
250 <223> OTHER INFORMATION: Description of Artificial Sequence:DNA coding for
251 amino acids SEQ ID No.2
253 <400> SEQUENCE: 5
254 atgcagcagc cttcaatta cccatatccc cagatctact gggtgacag cagtccagc 60
255 tctccctggg cccctccagg cacagttctt ccctgtccaa cctctgtgcc cagaaggcct 120
256 ggtcaaagga ggccaccacc accaccgcca ccgcaccac taccacctcc gccgcgcgg 180
257 ccaccactgc ctccactacc gctgccaccc ctgaagaaga gagggAACCA cagcacaggc 240
258 ctgtgtctcc ttgtatgtt ttcatgtt ctgggtgcct tgtaggatt gggctgggg 300
259 atgttcagc tctccaccc acagaaggag ctggcagaac tccgagatc taccagccag 360
260 atgcacacag catcatctt ggccacccc agtccacccc ctgaaaaaaaaa ggagctgagg 420
261 aaagtggccc attaacagg caagtccaa tcaaggcca tgcctctgg atggaaagac 480
262 acctatggaa ttgtccctgct ttctggatgt aagtataaga agggtgccct tttgtatcaat 540
263 gaaactgggc ttttactttgtt atattccaaa gtataactcc ggggtcaatc ttgcaacaac 600
264 ctggccctga gccacaaggctt ctacatgagg aactctaagt atccccagga tctgggtatg 660
265 atggagggggaa agatgtatgag ctactgcact actgggcaga tttggggccctt cagcagctac 720
266 ctggggggcag ttttcaatctt taccatgtctt gatcattttat atgtcaacgt atctgagctc 780
267 tctctggtca attttgagga atctcagacg ttttcggct tatataagct c 831
270 <210> SEQ ID NO: 6
271 <211> LENGTH: 843

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Input Set : A:\2003-06-09 1110-0266P.ST25.txt
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272 <212> TYPE: DNA
 273 <213> ORGANISM: Artificial Sequence
 275 <220> FEATURE:
 276 <223> OTHER INFORMATION: Description of Artificial Sequence:DNA coding for
 277 amino acids SEQ ID No.3
 279 <400> SEQUENCE: 6
 280 atgcagcagc cttcaatta cccatatccc cagatctact gggtggacag cagtgccagc 60
 281 tctccctggg cccctccagg cacagttttt ccctgtccaa cctctgtgcc cagaaggcct 120
 282 ggtcaaaaggga ggccaccacc accaccgcca ccgcaccac taccacctcc gccgcccgg 180
 283 ccaccactgc ctccactacc gtcgacccctt ctgaagaaga gagggAACCA cagcacaggc 240
 284 ctgtgtctcc ttgtatgtt tttcatgggtt ctgggtgcct tggttaggatt gggcctgggg 300
 285 atgtttcagc tcttccacctt acagaaggag ctggcagaac tccgagagtc taccagccag 360
 286 atgcacacag catcatcttt ggaggcacaat agggccacc ccagtccacc ccctgaaaaa 420
 287 aaggagctga ggaaagtggc ccatttaaca ggcaagtcca actcaaggc catgcctctg 480
 288 gaatgggaag acacccatgg aattgtcccg ctccctggag tgaagtataa gaagggtggc 540
 289 ctgtgtatca atgaaactgg gctgtacttt gtatattcca aagtataactt ccgggggtcaa 600
 290 tcttgcaaca acctggccct gagccacaag gtctacatga ggaactctaa gtatccccag 660
 291 gatctggta tgatggaggg gaagatgtt agctactgca ctactggca gatgtgggc 720
 292 cgcagcagctt acctgggggc agtgttcaat cttaccatgt ctgtatcattt atatgtcaac 780
 293 gtatctgagc tctctcttgtt caatggatcaga cggtttcgg cttatataag 840
 294 ctc 843
 296 <210> SEQ ID NO: 7
 297 <211> LENGTH: 20
 298 <212> TYPE: DNA
 299 <213> ORGANISM: Artificial Sequence
 301 <220> FEATURE:
 302 <223> OTHER INFORMATION: Description of Artificial Sequence:a sense primer
 303 BOS6
 305 <400> SEQUENCE: 7
 306 cctcagacag tggttcaaag 20
 309 <210> SEQ ID NO: 8
 310 <211> LENGTH: 39
 311 <212> TYPE: DNA
 312 <213> ORGANISM: Artificial Sequence
 314 <220> FEATURE:
 315 <223> OTHER INFORMATION: Description of Artificial Sequence:an antisense
 316 deletion primer DA4
 318 <400> SEQUENCE: 8
 319 ttttcagggg gtggactggg ctccttctgtt aggttggaaag 39
 322 <210> SEQ ID NO: 9
 323 <211> LENGTH: 28
 324 <212> TYPE: DNA
 325 <213> ORGANISM: Artificial Sequence
 327 <220> FEATURE:
 328 <223> OTHER INFORMATION: Description of Artificial Sequence:HFLP3
 330 <400> SEQUENCE: 9
 331 gctctagaac attctcggtt cctgttaac . 28
 334 <210> SEQ ID NO: 10
 335 <211> LENGTH: 30

VERIFICATION SUMMARY

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